

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: March 17, 2003, 08:47:56 ; Search time 22 Seconds  
(without alignments)  
339,663 Million cell updates/sec

Title: US-10-010-227-3  
Perfect score: 4055  
Sequence: 1 MPAESTPQTLVDKVLQAHV.....KAVPPTNKGKKEPLEW 778

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2473.5	61.0	758	2 T39210	3-isopropylmalate
2	2456.5	60.6	779	2 S64011	3-isopropylmalate
3	2366	58.3	689	2 S26864	3-isopropylmalate
4	2076	51.2	644	2 UQ0160	3-isopropylmalate
5	1611	39.7	469	2 AH3271	3-isopropylmalate
6	1586	39.1	475	2 C97684	2-isopropylmalate
7	1584	39.1	469	2 AD2909	3-isopropylmalate
8	1562	38.5	479	2 C87273	3-isopropylmalate
9	1548.5	38.2	469	2 G81128	3-isopropylmalate
10	1545.5	38.1	469	2 A81836	probable 3-isoprop
11	1507.5	37.2	474	2 G83255	3-isopropylmalate
12	1498.5	37.0	474	2 H82564	3-isopropylmalate
13	1479.5	36.5	466	2 H64728	3-isopropylmalate
14	1477.5	36.4	466	2 AD0516	3-isopropylmalate
15	1471	36.3	469	2 F64163	3-isopropylmalate
16	1469.5	36.2	466	2 D80638	hypothetical prote
17	1469.5	36.2	466	2 D85489	3-isopropylmalate
18	1452	35.8	476	2 A10065	3-isopropylmalate
19	1425.5	35.2	467	2 H82070	3-isopropylmalate
20	1413	34.8	485	2 T13699	3-isopropylmalate
21	1396	34.4	472	2 H84031	3-isopropylmalate
22	1393.5	34.4	472	2 B69650	3-isopropylmalate
23	1385.5	34.2	476	2 T29083	3-isopropylmalate
24	1385	34.2	473	2 G70883	probable leuc prot
25	1354	33.4	476	2 T45425	3-isopropylmalate
26	1354	33.4	485	2 G87119	3-isopropylmalate
27	1311.5	32.3	470	2 A81270	3-isopropylmalate
28	1304.5	32.2	464	2 S10171	3-isopropylmalate
29	1283.5	31.7	462	2 AF1694	3-isopropylmalate
30	1282	31.6	456	2 A89998	3-isopropylmalate
31	1279.5	31.6	462	2 AE1323	3-isopropylmalate
32	1181.5	29.1	468	2 S76826	hypothetical prote
33	1172.5	28.9	467	2 AF1983	3-isopropylmalate
34	1141.5	28.2	460	2 S35134	probable 3-isoprop
35	1132.5	27.9	459	2 D86777	hypothetical prote
36	1114	27.5	460	2 D36889	3-isopropylmalate
37	684.5	16.9	422	2 C70381	large subunit of i
38	662.5	16.3	267	2 T39573	probable 3-isoprop
39	641	15.8	431	2 H75354	3-isopropylmalate
40	640.5	15.8	659	2 F70453	aconitase - Aquife
41	637.5	15.7	423	2 B75045	probable 3-isoprop
42	635	15.7	424	2 D64362	aconitase hydrat
43	613	15.1	419	2 D69051	3-isopropylmalate
44	602.5	14.9	420	2 B64425	3-isopropylmalate
45	599	14.8	642	2 H97019	aconitase A (impor
46	597.5	14.7	211	2 AB3561	3-isopropylmalate
47	595.5	14.7	417	2 H72362	3-isopropylmalate
48	587.5	14.5	433	2 B69495	aconitase (acn) ho
49	576.5	14.2	422	2 C97280	3-isopropylmalate
50	573.5	14.1	436	2 G69524	aconitase (impor
51	562	13.9	661	2 H84406	3-isopropylmalate
52	560.5	13.8	216	2 F97693	3-isopropylmalate
53	558.5	13.8	201	2 AE2919	3-isopropylmalate
54	558.5	13.8	509	2 T06380	hypothetical prote
55	552	13.6	428	2 A69085	3-isopropylmalate
56	552	13.6	721	2 T38665	probable homoeconi
57	544	13.4	213	2 C81836	3-isopropylmalate
58	542	13.4	212	2 F83255	3-isopropylmalate
59	542	13.4	213	2 E81128	3-isopropylmalate
60	541.5	13.4	418	2 C72384	hypothetical prote
61	532.5	13.1	693	1 S61067	homoeconitase hydr
62	519	12.8	215	2 G82564	3-isopropylmalate
63	513	12.7	202	2 B87273	3-isopropylmalate
64	512	12.6	434	2 D75373	3-isopropylmalate
65	506	12.5	201	2 AC0516	3-isopropylmalate
66	505	12.5	201	2 S07306	3-isopropylmalate
67	498	12.3	200	2 A82071	3-isopropylmalate
68	495	12.2	200	1 G64106	3-isopropylmalate
69	492	12.1	201	2 C90638	3-isopropylmalate
70	492	12.1	201	2 C85489	isopropylmalate is
71	491	12.1	201	2 S40585	3-isopropylmalate
72	482.5	11.9	191	2 E36889	probable 3-isoprop
73	482.5	11.9	780	2 T52533	aconitase hydrat
74	475	11.7	208	2 S44831	aconitase hydrat
75	474	11.7	200	2 AH0065	F4H12.1 protein -
76	467	11.5	194	2 G84031	3-isopropylmalate
77	466.5	11.5	199	2 C69650	3-isopropylmalate
78	462.5	11.4	781	2 A35584	aconitase hydrat
79	447.5	11.0	789	2 S57528	aconitase hydrat
80	444.5	11.0	789	2 S65631	aconitase hydrat
81	443.5	10.9	779	2 S57805	aconitase hydrat
82	439.5	10.8	778	2 T38347	aconitase hydrat
83	434.5	10.7	778	2 S50387	aconitase hydrat
84	422	10.4	200	2 H81269	probable 3-isoprop
85	421	10.4	190	2 B89998	3-isopropylmalate
86	417	10.3	416	2 A99419	hypothetical prote
87	394.5	9.7	870	2 T27868	hypothetical prote
88	393	9.7	870	2 T39571	probable aconitase
89	387	9.5	208	2 G19571	aconitase hydrat
90	386.5	9.5	906	2 G75362	aconitase hydrat
91	386	9.5	137	2 S43885	3-isopropylmalate
92	384.5	9.5	895	2 A13483	aconitase hydrat
93	384.5	9.5	910	2 B83451	aconitase hydrat
94	384	9.5	868	2 B82213	aconitase hydrat
95	384	9.5	907	2 T04820	aconitase hydrat
96	375.5	9.3	193	2 A11323	3-isopropylmalate
97	375	9.2	386	2 T51171	homoeconitase hydr
98	369.5	9.1	903	2 A87704	aconitase hydrat
99	366.5	9.1	193	2 AG1694	3-isopropylmalate
100	366	9.0	898	2 T10101	aconitase hydrat



```

|||||
Db 129 GFTLPSTVVCSSHTSTHGAFGSLAFGIGTSEVHVLAOTITIIQAKSKMRRITVNGKLS 188
Qy 188 PGVSKSVVLAIGIIGTAGGTGAVIEFCGSVSIISMSEAMSICNMSIEGGARAGMVP 247
Db 189 PGTSKDLITITIGLIGTAGTGCVIEFAGAEIETLSMEANSMCNMAIEGARGMIRP 248
Qy 248 DELTEYLKGRPLAPKYDSPEMHKAQYWKNLQSDPGAKYDIDVFIDAKDIPVTLTWGTS 307
Db 249 DELTFOYTKGRPLAPK--GAEMEKAVAWYKTLKTDGAKFDEHINIEAVDIPIITWGST 306
Qy 308 PEDVVPITGVVPEDETFATEAKKADGRMLQYMGKAGTPEMDIPVDKVFISGCTNSIE 367
Db 307 PODALPITGSVPDEPKNVTPDIKSGMERALAYMGLEPNTPLKSIIVDVDFISGCTNGRIE 366
Qy 368 DLRAAAVVKGRKAPNVKSAMVVPGSGLVKTOAEEGDKIFEEAGFEMWEGAGSMCLG 427
Db 367 DLRAAAVVKGRKQKLAISNIKLAHVPGSGLVKQAEAGLDIKI FQAGFEMWEGAGSICLG 426
Qy 428 MNPDIAPQERCASTSNRNFEGRGAGRTHLMSPVMAAAGIVGLADVRLTDYK-- 484
Db 427 MNPDIILAYEHCASSTNNFEGRGALSRTHLMSPMAAAGIAGHPVDIREF--EYKQD 485
Qy 485 -ASPHI-----AAVQKSTVTKPHVDERINDQAEKDIADIPEDNNGPHNTS 531
Db 486 QSSPKVEVTSDEKELESAAVDHAEVPQ--EDAPQDI--ANDELDKIPVXSDDTPAKPS 541
Qy 532 ASVTSAGLPFTTLKGIAPLEKANVDTDAIIPKQFLKTKRTGLGNALFPEWKFENEDG 591
Db 542 ----SSGMKFLTELEGISAPLDKANVDTDAIIPKQFLTKRTGLKGLFPEWFRKOD 596
Qy 592 ----TEKSDVFNKEPYRKASILVCTGANFGCGSSREHAPMALNDFGIRSVIAPSPADIFF 648
Db 597 QGKQGEITDFVNVPEWRRAELIVTGNFGCGSSREHAPMALNDFGIRSVIAPSPADIFF 656
Qy 649 NNSFRKGMPLPIPKQAOQIEAIAEAPAKGEIEVDLPNOLIKNATGETITCT--FEVIEBRK 707
Db 657 NNSFRKGMPLPIRLDQOIITDKLIPYANKGKGLCVLDLPNOKIUDSGNVLVHDFEIEPFRK 716
Qy 708 HCLVNGLDIDIGLTMQMEKIAFEFAKMTRETPWLDGTGL-----KRK 750
Db 717 HCLVNGLDIDIGLITQKEEYISRYEALRREKYSFLEGSKLKFQNVNPKK 766

RESULT 3
3-Isopropylmalate dehydratase (EC 4.2.1.33) - Phycomyces blakesleanus
N:Alternate names: alpha-IPM isomerase; alpha-Isopropylmalate isomerase
C:Species: Phycomyces blakesleanus
C>Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 17-Mar-2000
C:Accession: S26864; S10998
R:Iturriaga, E.A.; Diaz-Minguez, J.M.; Benito, E.P.; Alvarez, M.I.; Esclava, A.P.
Curr. Genet. 21, 215-223, 1992
A:Title: Heterologous transformation of Mucor circinelloides with the Phycomyces blakesleanus
A:Reference number: S26864; MUID:92224296; PMID:1563047
A:Accession: S26864
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-689 <ITV>
R:Iturriaga, E.A.; Diaz-Minguez, J.M.; Benito, E.P.; Alvarez, M.I.; Esclava, A.P.
Nucleic Acids Res. 18, 4612, 1990
A:Title: Nucleotide sequence of the Phycomyces blakesleanus leu1 gene.
A:Reference number: S10998; MUID:90356419; PMID:2388845
A:Accession: S10998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-689 <ITV>
A:Cross-references: EMBL:X53090; NID:g3112; PIDN:CAA37257.1; PID:g3113
C:Genetics:
A:Gene: leu1
C:Superfamily: homoaconitate hydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase; leucine biosynthesis

```

```

Query Match 58.3%; Score 2366; DB 2; Length 689;
Best Local Similarity 68.4%; Pred. No. 1,4e-157;
Matches 472; Conservative 62; Mismatches 132; Indels 24; Gaps 9;

Qy 9 QTLVDKVLQAHVNDKLDGTVLAIYIDRHLVHEVTSPOAFEGELRNAGRKVRPDDTLATTD 68
Db 3 RTLDKVDWHDV-----IDRLVHEVTSPOAFEGELRNARVRPDDTLATVD 50
Qy 69 HNVPTTSRKALKDIASTFKEDDSRTQCVTLEENYKEFGVTYFGLSDKRQGIYVHYIGPEQG 128
Db 51 HNIPPTFRKFKFSITTFIDEADSRQCELTETNVKEFELTFYEGMEDSRQGIYVHYIGPEQG 110
Qy 129 FTLPGETVVCSDSTHTSHGAFGALAFGISTSEVHVLAOTGLIKRSKNMRIOVDGELAP 188
Db 111 FTLPGETVVCSDSTHTSHGAFGALAFGISTSEVHVLAOTGLIKRSKNMRIOVDGELAP 170
Qy 189 GVSSKDVVLAIGIIGTAGGTGAVIEFCGSVSIISMSEARMSICNMSIEGGARAGMVPAD 248
Db 171 GVTSKDVVLAHYIGLITAGTRCVIEFGSAIASISMSEARMSICNMSIEGGARAGMVPAD 230
Qy 249 EITFEYLKGRPLAPKYDSPEMHKAQYWKNLQSDPGAKYDIDVFIDAKDIPVTLTWGTS 308
Db 221 EITFEYLKGRPLAP--EGAEWDKAVQYKSLKSDPNAKYDIDVXIAASDIAPITITWGTSP 288
Qy 309 EDVVPITGVVPEDETFATEAKKADGRMLQYMGKAGTPEMDIPVDKVFISGCTNSRIED 368
Db 289 QDVAPITGVVPEDETFATEAKKADGRMLQYMGKAGTPEMDIPVDKVFISGCTNSRIED 348
Qy 369 LRAAAVVKGRKAPNVKSAMVVPGSGLVKTOAEEGDKIFEEAGFEMWEGAGSMCLGM 428
Db 349 LRSASIVKGRKADNV--YAVVPGSGLVKQAELEGIDKFTPDGAFEMWEGAGSMCLGM 407
Qy 429 NPDILAPQERCASTSNRNFEGRGAGRTHLMSPVMAAAGIVGLADVRLTDYKASPH 488
Db 408 NPDQSPBERCASTSNRNFEGRGAGRTHLMSPVMAAAGIIRGYLTDYKASPH 467
Qy 489 IAAVQKSTVTKPHVDERI--NDAHEKDIADIPEDNNGPHNTSASVGTSGLKFTTL 546
Db 468 SPPPKFQTI--QPKVDEAAHKQADQADPVTDCEP--AGSPVNGAPV--ASAMAPFTTL 522
Qy 547 KGIAAPLEKANVDTDAIIPKQFLKTKRTGLGNALFPEWKFENEDGTEKSDVFNKEPYR 605
Db 523 KGVAAAPLAISNVDIMMILPKQFLKTKRTGLGSLALFYGIRYDPAIGAERKPDVNLQPAIR 582
Qy 606 KASILVCTGANFGCGSSREHAPMALNDFGIRSVIAPSPADIFFNNSFKXGMLPIPKQQA 665
Db 583 SSKILVCTGANFGCGSSREHAPMALNDFGIRSVIAPSPADIFFNNSFKXGMLPI--ILSQE 641
Qy 666 QIEAIAEAPAKGEIEVDLPNOLIKNATGE 695
Db 642 QVDTLAKYATQAEIEVDLVHOKIRYPGGE 671

RESULT 4
3-Isopropylmalate dehydratase (EC 4.2.1.33) - Rhizomucor circinelloides
N:Alternate names: alpha-Isopropylmalate isomerase
C:Species: Rhizomucor circinelloides
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Mar-2000
C:Accession: J00160; S26865
R:Romero, M.I.G.; Jepsen, L.P.; Stroman, P.; van Heeswijk, R.
Gene 84, 335-343, 1989
A:Title: Characterization of a leuA gene and an ARS element from Mucor circinelloides.
A:Reference number: J00160; MUID:90128278; PMID:2693214
A:Accession: J00160
A:Molecule type: DNA
A:Residues: 1-644 <RON>
A:Cross-references: GB:M33166; NID:g168366; PIDN:AAA33422.1; PID:g168367
A>Note: The authors translated the codon ATT for residue 119 as Asn
R:Iturriaga, E.A.; Diaz-Minguez, J.M.; Benito, E.P.; Alvarez, M.I.; Esclava, A.P.
Curr. Genet. 21, 215-223, 1992
A:Title: Heterologous transformation of Mucor circinelloides with the Phycomyces blakesleanus
A:Reference number: S26864; MUID:92224296; PMID:1563047

```

A:Accession: S26865  
A>Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-644 <ITU>  
C:Comment: This enzyme is involved in the biosynthesis of leucine.  
C:Genetics:  
A:Gene: leuA  
C:Superfamily: homoaconitate hydratase  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 51.2%; Score 2076; DB 2; Length 644;  
Best Local Similarity 68.8%; Pred. No. 2.6e-137;  
Matches 407; Conservative 60; Mismatches 111; Indels 14; Gaps 6;

QY 10 TLYDKVLQAHVVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCTLATTDH 69  
DB 51 TLYDKVMDHVDIQOEDGTCLYIDRHLVHEVTSPOAFEGRLNANRPVRRPDCTLATVDH 110  
QY 70 NVPTTSRKALKDIASFKEKDDSRTOCVTLEENVKEFGVYFGLSDKROGIVHVIGPEQGF 129  
DB 111 NIPITTRKIFKNITTFIKEADSRTOCVTLEENVKEFGVYFGLSDKROGIVHVIGPEQGF 170  
QY 130 TLPGTTVVCDSHTSTHGAFAFGAGTSEVHVLATQCLITKRSKMRIOVDGELAPG 189  
DB 171 TLPATVVCDSHTSTHGAFAFGAGTSEVHVLATQCLITKRSKMRIRVOGKALPG 230  
QY 190 VSKDVLVLAIGTAGGTGAVTEFCGVSIRLSMEARMSICNMSIEGGARAGVAPDE 249  
DB 231 VTSKDVLVLTIGVITAGGTGCVIEFCGDTTAAALSMESRMSICNMSIEAGARAGVAPDE 290  
QY 250 ITEFLYKGRPLAPKYDSEPHKATQYWKNLQSDPGAKYDIDVFDKADIVPTLTWGSPE 309  
DB 291 VTPEYLRDKPLAPK--GADWDRAVKKYKSLSSDADAKYDINVEAADIAPLTWTGTSQP 348  
QY 310 DVVPIITGVVDPDPTFAEAKKADGRMLQYMGKAGTPEMIDPVDFKFGISCTNSRIEDL 369  
DB 349 DVVPIITGSTPDKIEDPIRRSAVQALDYIGIAPNTPMEGVKVDKVFISCTNSRIEDL 408  
QY 370 RAAAVVKKRKKAPNVKSAVVPGSLVKTQAELEGDKIFEEAGFBEWRAGCSMCLGMN 429  
DB 409 RAAAVVKKRRAAEWV--DAMVVPGLVKKRAEREGLDKIPTDAGFDWRAGCSMCLGMN 467  
QY 430 PDTLAPQERCASTSNRNFEGRQAGGRTHLMSPVMAAAGIVGKLADVRKLTIDYKASPHI 489  
DB 468 PDQLKEGERCASTSNRNFEGRQAGGRTHLVSPMAAAGIKGCLTDVRRNN-----EV 520  
QY 490 AAYQKSTVTKPHYDERINODAEKDIADIPEDNNGPHTNTSASVGTSAGLPKFTILKGI 549  
DB 521 SEIPGTPKQSPRQEVVAEFSEEDV--DSSSVDSAP-VATPPSTGDSAGMPKFTILKGY 577  
QY 550 AAPLEXANVDTDAIIPKQFLTKTKRTGLGNALFYEMRFN-EDGTEKSDFVLN 600  
DB 578 AAPLDISNVDTDAIIPKQFLTKTKRTGLGALFYALFDPATGAENPDFVLN 629

RESULT 5  
AH3271  
3-isopropylmalate dehydratase (EC 4.2.1.33) [imported] - Brucella melitensis (strain 16M)  
C:Species: Brucella melitensis  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 03-Jun-2002  
C:Accession: AH3271  
R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A:Reference number: AB3252; PMID:11756688  
A:Accession: AH3271  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-469 <KUR>  
A:Cross-references: GB:AE008917; PIDN:AAL51339.1; PID:gl7982037; GSPDB:GN00190  
A:Experimental source: strain 16M  
C:Genetics:

A:Gene: BMEI0157  
A:Map position: 1  
C:Superfamily: aconitate hydratase  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 39.7%; Score 1611; DB 2; Length 469;  
Best Local Similarity 66.8%; Pred. No. 5.9e-105;  
Matches 316; Conservative 51; Mismatches 98; Indels 8; Gaps 3;

QY 6 STPQTLYDKVLQAHVVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCTLA 65  
DB 2 SAPRTLYDKIWDHVDVQOEDGTCLYIDRHLVHEVTSPOAFEGRLNAGRPVHPKXTLA 61  
QY 66 TTDHNVPTTSRKALKDIASFKEKDDSRTOCVTLEENVKEFGVYFGLSDKROGIVHVIGP 125  
DB 62 VVDHNVPTS-----PDRINGIQNEESRIQVEALARNADFGVEYSERDKROGIVHVIGP 116  
QY 126 EOGFTLPGTIVCGDSHTSTHGAFAFGAGTSEVHVLATQCLITKRSKMRIOVDGE 185  
DB 117 EOGFTLPGMTIVCGDSHTSTHGAFAFGAGTSEVHVLATQCLITKRSKMRIOVDGK 176  
QY 186 LAPGVSSKDVVLHAIGTAGGTGAVTEFCGVSIRLSMEARMSICNMSIEGGARAGV 245  
DB 177 LPAGVTAQDVLAIIGTAGGTGAVTEFCGVSIRLSMEARMSICNMSIEGGARAGLI 236  
QY 246 APDETTFEYLKGRPLAPKYDSEPHKATQYWKNLQSDPGAKYDIDVFDKADIVPTLTW 305  
DB 237 APDETTFEYLKGRPRAPQOETLE--QAINYWKTLHSDGAHPDKIVTLDAGSLPPIVSMG 294  
QY 306 TSPEDVPIITGVVDPDPTFAEAKKADGRMLQYMGKAGTPEMIDPVDFKFGISCTNSR 365  
DB 295 SSPEDVSVITGVVPPNDIADETKRAKRWALDYGLKPGTKITDIAVDRVFGISCTNGR 354  
QY 366 IEDLRAAAAVKGRKKAPNVKSAVVPGSLVKTQAELEGDKIFEEAGFBEWRAGCSMC 425  
DB 355 IEDLRAAAVKEGKVAQTV-NAMIVPGSLVKEQAELEGDKIFEEAGFBEWRAGCSMC 413  
QY 426 LGMPDILAPQERCASTSNRNFEGRQAGGRTHLMSPVMAAAGIVGKLADVR 478  
DB 414 LAMNDRLLKPGERCASTSNRNFEGRQAGGRTHLVSPMAAAGIAGHFVDIR 466

RESULT 6  
C97684  
2-isopropylmalate isomerase large chain (AJ236268) [imported] - Agrobacterium tumefaciens  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
C:Accession: C97684  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A:Reference number: A97359; PMID:11743194  
A:Accession: C97684  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-475 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AAK88428.1; PID:gl5157923; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR C 4910  
A:Map position: circular chromosome  
C:Superfamily: aconitate hydratase

Query Match 39.1%; Score 1586; DB 2; Length 475;  
Best Local Similarity 65.3%; Pred. No. 3.4e-103;  
Matches 311; Conservative 52; Mismatches 105; Indels 8; Gaps 3;  
QY 4 AESTPQTLYDKVLQAHVVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCT 63  
DB 6 AMSAPRTLYDKIWDHVVNRPDGTCLYIDRHLVHEVTSPOAFEGRLIAGRPVHSPFTR 65  
QY 64 LATTDHNVPTTSRKALKDIASFKEKDDSRTOCVTLEENVKEFGVYFGLSDKROGIVHVI 123  
DB 64 LATTDHNVPTTSRKALKDIASFKEKDDSRTOCVTLEENVKEFGVYFGLSDKROGIVHVI 123

Db 66 LAVVDHNVPTTA-----DRLEGIKNESRIQVEALAAQNAKERGVYSEBRDQGIYVHT 120

Qy 124 GPEQGTLPCTTVCGBSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIOVD 183

Db 121 GPEQGTLPCTTVCGBSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIOVD 180

Qy 184 GELAPGVSSKDVVLAIGITAGTGAIVIEFCGSVIRSLSMSEARMSICNMSIEGGARPG 243

Db 181 GKLPESYATADIIAIIIGETAGTGIVIEFAGAIRSLSMSEGMTVCNMTIEGGARAG 240

Qy 244 MVNPDEITFEYLKGRPLAPKYDSPEMHKATQYWKULQSDPGAKYDIDVDFDAKDIPTLT 303

Db 241 LIAPDEITFDITKGRPRAPKGETLE--QAIAYWKTLSDEGAHYDKVVLIDANLPIIVS 298

Qy 304 WGTSPEDVPTTGVVPPETPATEAKKADGRRLQYMGAKAGTPEMDIPVDKVFISGCTN 363

Db 299 WGTSPEDVPTTGVVPPETPATEAKKADGRRLQYMGAKAGTPEMDIPVDKVFISGCTN 358

Qy 364 SRLEDLRAAAAVVGRKKAPVYKAMVYPSGLVYKTOAEBSGLDKIFEEAGFEWREAGCS 423

Db 359 GRLEDLRAAAAVVGRKKAPVYKAMVYPSGLVYKTOAEBSGLDKIFEEAGFEWREAGCS 417

Qy 424 MCGMNPDIILAPORCASTSNRNFEGRGAGGRTHLMSPVMAAAAGIVGKLADVRK 479

Db 418 MCLAMNDRLKGERCASTSNRNFEGRGAGGRTHLMSPVMAAAAGIVGKLADVRK 473

RESULT 7

3-isopropylmalate dehydratase, large subunit [imported] - Agrobacterium tumefaciens (str AD2909

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002

C/Accession: AD2909

R/Mod: D.W.; Secubai, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutuyarin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreppan, W.; Perry, M.; Gordon-Kamm, ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB25777; PMID:11743193

A/Accession: AD2909

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-469 <KOR>

A/Cross-references: GB:AE008688; PIDN:AL143690.1; PID:g17741217; GSPDB:GN00186

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Gene: leuc

A/Map position: circular chromosome

C/Superfamily: aconitate hydratase

Query Match 39.1%; Score 1584; DB 2; Length 469;

Best Local Similarity 65.4%; Pred. No. 4.6e-103;

Matches 310; Conservative 52; Mismatches 104; Indels 8; Gaps 3;

Qy 6 STPCTLYDKVLAHVVDKLDGTVLYTIDRHLVHEVTSPOAFEGELNARKVRRPDCITLA 65

Db 2 SAPRTLYDKIMDDHVNKDPDGTCLLYIDRHLVHEVTSPOAFEGELNARKVRRPDCITLA 61

Qy 66 TTDHNVPTTSRKALKDIAFIKEDDSRTQCVTLSENVKEFGVTYFGLSDRKQGIYVHT 125

Db 62 VVDHNVPTTA-----DRLEGIKNESRIQVEALAAQNAKERGVYSEBRDQGIYVHT 116

Qy 126 EOGTLPCTTVCGBSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIOVD 185

Db 117 EOGTLPCTTVCGBSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIOVD 176

Qy 186 LAPGVSSKDVVLAIGITAGTGAIVIEFCGSVIRSLSMSEARMSICNMSIEGGARAG 245

Db 177 LPESYATADIIAIIIGETAGTGIVIEFAGAIRSLSMSEGMTVCNMTIEGGARAG 236

Qy 246 APDEITFEYLKGRPLAPKYDSPEMHKATQYWKULQSDPGAKYDIDVDFDAKDIPTLT 305

Db 237 APDEITFDITKGRPRAPKGETLE--QAIAYWKTLSDEGAHYDKVVLIDANLPIIVS 294

Qy 306 TSPEDVPTTGVVPPETPATEAKKADGRRLQYMGAKAGTPEMDIPVDKVFISGCTNSR 365

Db 295 TSPEDVPTTGVVPPETPATEAKKADGRRLQYMGAKAGTPEMDIPVDKVFISGCTNSR 354

Qy 366 IEDLRAAAAVVGRKKAPVYKAMVYPSGLVYKTOAEBSGLDKIFEEAGFEWREAGCS 425

Db 355 IEDLRAAAAVVGRKKAPVYKAMVYPSGLVYKTOAEBSGLDKIFEEAGFEWREAGCS 413

Qy 426 LGMNPDIILAPORCASTSNRNFEGRGAGGRTHLMSPVMAAAAGIVGKLADVRK 479

Db 414 LGMNPDIILAPORCASTSNRNFEGRGAGGRTHLMSPVMAAAAGIVGKLADVRK 467

RESULT 8

3-isopropylmalate dehydratase, large subunit [imported] - Caulobacter crescentus C87273

C/Species: Caulobacter crescentus

C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001

C/Accession: C87273

R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolm n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A/Title: Complete Genome Sequence of Caulobacter crescentus.

A/Reference number: A87249; PMID:1173698; PMID:11259647

A/Accession: C87273

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-479 <STO>

A/Cross-references: GB:AE005673; NID:g13421319; PIDN:AAK2183.1; GSPDB:GN00148

C/Genetics:

A/Gene: CC0196

C/Superfamily: aconitate hydratase

Query Match 38.5%; Score 1562; DB 2; Length 479;

Best Local Similarity 64.4%; Pred. No. 1.6e-101;

Matches 307; Conservative 53; Mismatches 105; Indels 12; Gaps 5;

Qy 9 QTYDKVLAHVVDKLDGTVLYTIDRHLVHEVTSPOAFEGELNARKVRRPDCITLA 68

Db 4 KTYDKVLAHVVDKLDGTVLYTIDRHLVHEVTSPOAFEGELNARKVRRPDCITLA 62

Qy 69 HNVPTTSRKALKDIAFIKEDDSRTQCVTLSENVKEFGVTYFGLSDRKQGIYVHT 128

Db 63 HNVPTTSRKALKDIAFIKEDDSRTQCVTLSENVKEFGVTYFGLSDRKQGIYVHT 119

Qy 129 FTLPCTTVCGBSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIOVD 188

Db 120 FTLPCTTVCGBSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIOVD 179

Qy 189 GVSCKDVVLAIGITAGTGAIVIEFCGSVIRSLSMSEARMSICNMSIEGGARAG 248

Db 180 GVSCKDVVLAIGITAGTGAIVIEFCGSVIRSLSMSEARMSICNMSIEGGARAG 239

Qy 249 EITFEYLKGRPLAPKYDSPEMHKATQYWKULQSDPGAKYDIDVDFDAKDIPTLT 308

Db 240 EITFEYLKGRPLAPKYDSPEMHKATQYWKULQSDPGAKYDIDVDFDAKDIPTLT 297

Qy 309 EDVPTTGVVPPETPATEAKKADGRRLQYMGAKAGTPEMDIPVDKVFISGCTNSR 368

Db 298 EDVPTTGVVPPETPATEAKKADGRRLQYMGAKAGTPEMDIPVDKVFISGCTNSR 357

Qy 369 LRAAAAVV-----GRKKAPVYKAMVYPSGLVYKTOAEBSGLDKIFEEAGFEWREAGCS 423

Db 358 LRAAAAVV-----GRKKAPVYKAMVYPSGLVYKTOAEBSGLDKIFEEAGFEWREAGCS 416

Qy 424 MCGMNPDIILAPORCASTSNRNFEGRGAGGRTHLMSPVMAAAAGIVGKLADVRK 480

Db 417 MCLAMNDRLKGERCASTSNRNFEGRGAGGRTHLMSPVMAAAAGIVGKLADVRK 473

## RESULT 9

G81128  
3-Isopropylmalate dehydratase, large chain NMB1036 [imported] - Neisseria meningitidis  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: G81128  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
A:Reference number: AB1000; MUID:20175755; PMID:10710307  
A:Accession: G81128  
A:Status: preliminary  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-469 <T>  
A:Cross-references: GB:AE002454; GB:AE002098; MID:g7226273; PIDN:AAAF41435.1; PID:g722627  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB1036  
C:Superfamily: aconitate hydratase

Query Match 38.2%; Score 1548.5; DB 2; Length 469;  
Best Local Similarity 63.6%; Pred. No. 1.4e-100;  
Matches 302; Conservative 62; Mismatches 102; Indels 9; Gaps

Qy	7	TPQTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPQAEGFLRNAGRKVRPPDCTLAT	66
Db	2	TAQTLYDKLWNSHVVEEDGTVLLYIDRHLVHEVTSPQAEGFLMAGRKLRIDSVVST	61

Qy	 :: :: :: ::	67 TDHNVPTTSRKALKDIAFIKEDDSRTQCVTLEENVKEFG-VTYFGLSKRQGIVHVIGP 125
Db	 :: :: :: ::	62 ADHNTPT-----GDWDKGTDPPISKQLVDTLDKNIEFGALAYFFPMCKGQGVHMGP 115

Qy	126 EQGFTLPGTTWCGDSHTSTHGAFALAGICTSEVHVLATCLITKSKNMRIQVDGE 185 
Db	116 EQCATLPGMTVCGDSHTSTHGAFALAHGICTSEVHTMATOCITAKSKSMLISVDGK 175 

**Qy** 186 LAPGVSSKDVLHAITGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNNMSIEGGARGMV 245  
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :  
**Db** 176 LKAGVTAKDVALYIIGIQITAGGTGVAIEFGCGAIRSLSMESRMTLCNMAIFAGARSGMV 235

Qy	246	APDEITFEYLKGRPLAPKYDPSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIIVPTLTWG 305
Db	236	AVDQTITDVVKDFAPEGEA--WDKAVEYWRTLVSDGAVFDKEFYRFAEDIEPQVTWG 293

[illegible]

Qy	366	I E D L R A A A V V K G R K K A P N V K S A M V V P G S G L V K T Q A E E B G L D K I F E E A G F W R E A G C S M C	425
Db	354	I E D L R E A A A I A K D R K A A N V Q R V L I V P G S G L V K E A E K G L D K I F I E A G F W R E P G C S M C	413

Qy 426 LGMNPDLAPQERCASTSNRNFEGROGAGGRTHLWSPVMAAAGIVGKLADVRL 480

Db 414 LAMNADRLTPGQRCASTSNRNFEGROGGRTHLVS PMAAAAAVTCGFTDIRMM 468

## RESULT 10

A81836  
 Probable 3-isopropylmalate dehydratase (EC 4.2.1.33) large chain NM1450 [imported] - Ne  
 C;Species: Neisseria meningitidis  
 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C;Accession: A81836  
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 S.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
 A;Reference number: A81775; MUID:20222556; PMID:10761919  
 A;Accession: A81836

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-469 <PAR>  
A;Cross-references: GB:  
A;Experimental source: s  
C;Genetics:  
A;Gene: leuC; NMA1450

Query Match	38.1%	Score 1545.5;	DB 2;	Length 469;
Best Local Similarity	63.4%	Pred. No. 2.3e-100;		
Matches 301; Conservative	62;	Mismatches 103;	Indels 9;	Gaps

Qy	7	TPQTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPOAFEGLRNAGRKVRPDPCTLAT	66
		:           :           :           :           :	
Db	2	TAQTLYDKLWNSHVREEDGTVLLYIDRHLVHEVTSPOAFEGLRNAGRKLWRIDSVVST	61

Qy 67 TDHNVPTTSRKALXDIASTFKEDDSRTQCVTLLENVKBFQ-VTVFGLSKRQGIHVHIGP 125  
Db 62 ADHNTPT-----GWMDKGIQDPI SKLVQDTLDKNIEFGALAVFFPMDFQGQGIHVHMG 115

Qy	126	EQGFTLPGTWVCGDSHTSTHGAFAGALFGICTSEVEHVLATQCITTKRSKNMRIQVDGE	1895
Db	116	EQGATLPGMTWVCGDSHTSTHGAFAGALHGICTSEVEHTMATQCITAKSKSMLTAVDGGK	175

Qy 186 LAPGVSSKDVLHAIIGIIPAGGTGAVIEFGCSVIRSISMEARMSICNNMSIEGGARAGMV 245

Dd 176 LKAGVTAKDVALYIIQIGIIPAGGTGVAIEFGGFAIRSISMEGRMTLCNNMAIEAGARSGMV 235

QY 246 APBEITFEYLKGRPLAPKPYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPFLTWTG 305

Db 236 AVQOTTIDYVKDKPFAPEGEA--WDKAVEYWRITLNSDEGAVDFKEYRFNAPDIEPQVTWG 293

	Qy	Db
306	TSPEDVPTGVVDPDETFAATEAKKADGRRLQYMGLKAGTPEMIDIPVDKVFIGSCTNSR	365
294	TSPFWLDTSSKVPNPAEETDPVKRSGMERALEYMGLEAGTPLNEIPVDITVFIGSCTNSR	353

Qy	366	IEDLR	AAAA	VV	KGR	KAP	NV	KSA	MM	VP	GS	GL	V	K	TQ	AE	EG	LD	K	FEE	AG	FE	WR	EA	GC	SM	425	
Db	354	VEDLR	AAAA	TA	KDR	KA	AN	VQ	RV	LI	VP	GS	GL	V	K	EQ	AE	EG	LD	K	FIE	AG	FE	WR	EA	GC	SM	413

Qy	426	LGWNPDI	LAPQER	CASTSN	RNFEG	RAGG	RTHL	MSPV	MAAA	AGIV	GKLAD	VRKL	480
Db	414	LAMNAD	RLTGQ	RCASTS	RNRNF	EGRG	QGRTH	LVSP	MAAA	AAAT	VTGP	FTDIR	468

## RESULT 11

G83255  
3-isopropylmalate dehydratase large subunit P3121 [imported] - Pseudomonas aeruginosa  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: G83255  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
adman, S.; Kuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; I  
.: Lory, S.; Olson, M.V.  
Nature 406. 959-964. 2000

A;Accession: G02253  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-474 <STO>  
A;Cross-references: GB:AE004736; G  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: leuC; PA3121  
C;Superfamily: aconitate hydratase

Query Match 37.2%; Score 1507.5; DB 2; Length 474;  
Best Local Similarity 62.5%; Pred. No. 1.1e-97;  
Matches 295; Conservative 61; Mismatches 113; Indels Gaps 2;

Nature 404, 502-506, 2000  
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
 A;Reference number: A81775; MUID:20222556; PMID:10761919  
 A;Accession: A81836



QY	9	QTLDPKQLQAVNDEKLDGVLITYIDRLVHEVTSPPAEGLRNAGKVRPPDCLTTD	68
QY	10	QTLDPKQLQAVNDEKLDGVLITYIDRLVHEVTSPPAEGLRNAGKVRPPDCLTTD	69
Db	4	KTLVDKLMDMHLVQQRDDGSAIITYIDRHLIHEVTSPPAEGLRNAGKVRPPDCLTTD	63
QY	69	HNVPETSRKALKDIASFIEKEDDSRTQCVTLEENYKEFVITYEGLSDRKQGIHVHIGPEQG	128
Db	64	HNVPETSTERKGGIAA-IADEVSRLLQVOTLDENEDDDGITEFKNMDVRQOGIVHVGPEQG	122
QY	129	FTLPBPTVVCDSSTSHHGAFGALFGIGTSEVEHHVLTATQCLIRKBSKNRMIOVDGELAP	188
QY	123	ATLPBGMVVCDSSTSHHGAFGALHGIGTSEVEHHVLTATQCLVAKKKNMVLKVEGRLPA	182
QY	189	GVSSKSDVLLHAIGIIGTAGTGAVIEFGSGYIRSLISMERNISICMSIEGGARAGWAPD	248
Db	183	GVTKADIVLANIGSIGTAGNGHAIIEFGASAIIRDLSIEGRNTICMSIEAGARVGLAVD	242
QY	249	EITEFYELKGRPLAKYDSEPEWHKATQYWKALQSDPKAIDYIDVETIDAKDIYPTLTWGTSP	308
Db	243	QKITDYVKGREFAP-SAEOWDOAVACWQGLVSPADAFETDVEELDAQIIRPOVSWGTSP	300
QY	309	EDDVPIIGVNVDEPENFAIEAKKADGRMLQYMGKAGTPMEDIPVDKVFISGCSNRIED	368
Db	301	EMVLAVDONVPDPARESPPIKRGSTIERALKYMGRLRPNQATIDIQLDKRFISGCSNRIED	360
QY	369	LRAAAAVVKGKKKAPNVKSAWVPGSGLVKTQAEIEGLDKIIEEAGFEWREAGGSMCLGM	428
Db	361	LRAAAVARGKRVATIKQALVVPGSGLVKEQAEKEGIDRFIEIEAGFEWREAGGSMCLGM	420
QY	429	NPDLLAPOERASTSNRNFEGROGAGGRTHLMSPPMAAAAGVGLAVRXL	480
Db	421	NPDRLESGEHCASTSNRNFEGROGAGGRTHLVSPMAAAAVNGAFDIVREL	472

**RESULT 12**

H82564  
3-isopropylmalate dehydratase large subunit XF2375 [imported] - Xylella fastidiosa (strain C) Specles: Xylella fastidiosa #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
C>Date: 18-Aug-2000  
C:Accession: H82564  
R:Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
Nature 406, 151-157, 2000  
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A>Note: for a complete list of authors see reference number A59328 below  
A:Accession: H82564  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-674 <SIM>  
A:Cross-references: GB:AE004047, GE:AE003849, NID:g9107548, PIDN:AA865174.1; GSPDB:GN001  
A:Experimental source: strain 9A5C  
R:Simpson, A.U.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B  
Rlones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carer, b  
as-Neto, E.; Docena, C.; El-Dorzy, H.; Facinani, A.P.; Ferreira, A.J.S.  
submitted to Genbank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn, M.C.; J  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kriesger, J.E.; Kuramae, E.E.; Laigret, I  
chado, M.A.; Medeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, J  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Mircetta, C.C.; Miyaki, C.Y.; Palmeiri, D./  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Sawassa  
Rodrigues, V.; Rosa, A.U. de W.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawassa  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF2375  
A:Superfamily: aconitate hydratase

Db	4	KTLYSKLMDIHEVARDDGSSLIYIDRHITHEVTSPPAEPFGLRAGPELYRKVANINATP	63
Qy	69	HNVPTRSKALKDIASEFIKEDDSRTQCVLIEENVKEFVTVFGLSDXROGIVHVI	128
Db	64	HNVPPTAEEROGSLTS-IATVTSRLQVCTIDENCDPDGIFEFKKNVDVROGI	122
Qy	129	FTLPGTTVCCGSDSHSTHGAIPGALAFGIITSEVEHVUATQCLITKRSKNRI	188
Db	123	ATLPGMTVVCSDSHSTHGAIPGALAHGIGTSEVEHVUATQCLVTKMKNQV	182
Qy	189	GVSCKDVLALIGITGATGAVIEFCGSVIRLSMEARMSIKNMSLEGARAGMTAP	248
Db	183	GVTRKQDVLALLIGITGAGGAVAFERSSGSTRALSWEGRTTCINMAITEAGAR	242
Qy	249	EITPEYIKGRPLARKYDPSPEWHKATQYWKILQSDPGAKYDIDVETIDAK	308
Db	243	EKTIQYHGFPAFK--GSDMDAAVAFAWRGLVSDPDHAFRVVLSAETIKPY	300
Qy	309	EDVVPITGVVPDEPETFATEAKKADGRMYLQYMGIKAGTPEMEDIPVDK	368
Db	301	EMWASAVQSVDPDERETDPVYKKESLIRALKYMGQPPMDPIRISIKLDR	360
Qy	369	LRAAAAVKGRKKKAPNPKSAMVVPVSGSLVTKQAEPEGIDKTFEEAGFEM	428
Db	361	LRAAAVVKGRKVASITVKQAMVVPVSGSLVYKQAEVEGIDKTFIEAGFEM	420
Qy	429	NPDILAQERCASTSNRNPFGROGAGGRTHLSPVMAAAAGIVKLDVRL	480
Db	421	NPDKLGGSEHCASTSNRNPBGROGIGGRTHLVSPAMAAAAAVAGHPVD	472

RESULT 13  
 H64728  
 3-isopropylmalate dehydratase (EC 4.2.1.33) alpha chain - Escherichia coli (strain K-12)  
 C|Species: Escherichia coli  
 C|Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C|Accession: H64728; S40586; S41198; S43708  
 R|Batterer, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col  
 A|Rose, D.J.; Mau, B.; Snao, Y.  
 Science 277, 1453-1462, 1997  
 A|Title: The complete genome sequence of Escherichia coli K-12.  
 A|Reference number: A64720; MUID:9742617; PMID:9278503  
 A|Accession: H64728  
 A|Status: nucleic acid sequence not shown; translation not shown  
 A|Molecule type: DNA  
 A|Residues: 1-466 <BIAT>  
 A|Cross-references: GB:EB00117; GB:U00096; NID:g1786250; PIDN:ANC73183.1; PID:g1786259;  
 A|Experimental source: strain K-12, substrain MG1655  
 R|Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Microbuc  
 Submitted to the EMBL Data Library, December 1992  
 A|Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2  
 A|Reference number: S40531  
 A|Accession: S40586  
 A|Molecule type: DNA  
 A|Residues: 1-70, 'G', '72-361, 'V', '363-466 <YUR>  
 A|Cross-references: EMBL:D10483; NID:G216434; PIDN:BA01341.1; PID:G216490  
 A|Experimental source: Escherichia coli K-12  
 R|Kittling, H.; Aoki, M.; Aoshima, M.; Hayashi, Y.; Ohba, M.; Yamagishi, A.; Wakagi, T.; Oe  
 Eur. J. Biochem. 220, 275-281, 1994  
 A|Title: Hydrophobic interaction at the subunit interface contributes to the thermostabil  
 A|Reference number: S41197; MUID:94164169; PMID:8119295  
 A|Accession: S41198  
 A|Molecule type: DNA  
 A|Residues: 1-204 <KIR1>  
 A|Cross-references: EMBL:D17631  
 A|Experimental source: strain K-12  
 R|Kittling, H.; Aoki, M.; Hayashi, Y.; Ohba, M.; Yamagishi, A.; Wakagi, T.; Oshima, T.  
 submitted to the EMBL Data Library, September 1993  
 A|Reference number: S43708  
 A|Accession: S43708  
 A|Molecule type: DNA  
 A|Residues: 1-73, 'G', '75-204 <KIR2>





Db	117	LTLPGMTIIVGDSNHTATGAFALAFIGISTEVEHILATQTLQARAKSMKIEVRKVAS	176
Qy	189	GVSSKDVVLAHIGIITGTGGTCAVIEFCGSVIRLSMEARMSIICNMSIEGARAQWAPD	248
Db	177	GIATKDIILAIIGKTYMGGTGHVVEFCGEAIODLSMEGRMTVCNNALIEWAKAGLIAPD	236
Qy	249	EITFEYLKGRPLAPKYDSPEMHKATQYMWNLQSDPAKXDIDVFIADKIDVPLITWTGSP	308
Db	237	ETTFAYLKDPRHAK--GKDMEDAVAYMFKLSDDDAEPDVTVLEKDLAPQWTWTNP	294
Qy	309	EDVVPITGVAPDPETFATEAKKADGRMLQYMGKTAGTFMEDIPVDKVFIGSCNSTRIED	368
Db	295	GQYISVNETIPNPEQMDPVQPSASAKALHYIGLEGNTMYKDIKVDQVFIGSCNSTRIED	354
Qy	369	LRAAAAVYKGRKKA.PNYKSAAMYVPGSGLYKTOAEEBGLDKTIEEAGFEWREAGCSMCLGM	428
Db	355	LRAAAAYMKRKKKADNVRILIVPGSGLYKEQAEKEGLDKIFIAAAGAEWNPQCSMCLGM	414
Qy	429	NPDILAQECCASTSNRNFEEGRQAGSRTILMS.PWMAAAGIVGKLADVRKLT	481
Db	415	NDNRLEGMWECASISNNRFEGRQGNRTHILVSPAAAGAGVGRKVDLRDVT	467

```

RESULT 16
D90638
hypothetical protein ECs0076 [imported] - Escherichia coli (strain O157:H7, substrain RMD
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: D90638
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
sasawara, N.; Yasunaga, T.; Kunihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90638
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-466 <HAY>
A:Cross-references: GB:BA000007; PIDN:BAB33499.1; PID:q13359532; GSPDB:GNO0154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs0076
C:Superfamily: aconitate hydratase

Query Match          36.2%; Score 1469.5; DB 2; Length 466;
Best Local Similarity 61.9%; Pred. No. 4,7e-95;
Matches 292; Conservative 59; Mismatches 112; Indels 9; Gaps 4;

QY 9 OTLYDENVLAHVDEKLDGTVLLYIDRHLVHEVTSPOAFEGIRNAGRKRRPDCIATTD 68
Db 3 KTLVEKLFDAHVVEENETPLLIIDRHLVHEVTSPOAFDGI RAHGRPVROPCKTFATMD 62

QY 69 HNVPTSRKALNDIASFIKEDSRTOCVTLEENYKEFVFTVFGLSDDKQGIYHVIGREG 128
Db 63 HNVSTQT-----KQINN-C-GEARIQMOELLKNCKEPEVELYDLNHPQGIYHVMPREG 116

QY 129 FTLPGTTVCGDSHTSHGAFGALAFGIGISEVHVLTQCLITRSKNMRIQVDELAP 188
Db 117 VTLPGTTVCGDSHTSHGAFGALAFGIGISEVHVLTQCLITRSKNMRIQVDELAP 176

QY 189 GVSSKDVVLAHAIIGTAGTGAVIEFCGSVYRSLSMERBSICNMSEGGARAGNVAD 248
Db 177 GITADIVLAIIGKTSAGTGAVIEFCGEAIRDLSEGRWTLICMALEMGAAGAGVAD 236

QY 249 EITFEYLGRPLAPKYDSPEMHKATQYKNLQSDPGAKYDIDVFIADKIDVTLTWTGSP 308
Db 237 EITFNVVKRGLAPK--GKPFDDAVAYMKTLOTDEGATFDIVVTLTQAEISIQVYMGTP 294

QY 309 EDVVPITGVVPPETATEKAKKADGRMLQYMGAKAGPMEDIPVDKVFISGCTNSRIED 368
Db 295 GOVIVSNDNIPODPASPADVERASAEKALAYMGKPGILLTLEVALIDKVFISGCTNSRIED 354

```

QY	369	LRAAAAYVKRKPAVKSAMVY	PGSLVYTKQAEELDIT	FEADAGEMAEACSCICM	428
Db	355	LRAAEIAKRYKVAFGVQ	-ALVYPGSPYKAQAEAGLDIT	FEAGFERMLPGSCNICM	413
QY	429	NPDLIAQECASSTNPNEFGRCAGR	TLTMSPVMAAAAGVGTADYKTL	480	
Db	414	MNDRLNGEKCASSTNNKNEFGRCGRG	TLTLPVPAAMAAAYVGHPRDITNTI	465	

RESULT 17  
D85489  
hypochemical protein leuc [imported] - Escherichia coli (strain O157:H7, substrain EDL933;  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C;Accession: D85489  
R;Perna, N.T.; Plunkett II, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
Miller, L.; Grotbeck, E.U.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: AB85480; MUID:21074935; PMID:11206551  
A;Accession: D85489  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1466 <STC>  
A;Cross-references: GB:AE005174; NID:G12512772; PIDN:AAG54376.1; GSPDB:GN00145; UMG6:Z006  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: leuc  
A;Superfamily: aconitate hydratase

Query Match	36.2%	Score 1469.5	DB 2	Length 466
Best Local Similarity	61.9%	Pred. No. 4.7e-95		
Matches 292	Conservative 59	Mismatches 112	Indels 9	Gaps 4
QY	9	QTLVYKVLQAHVVDKLDGTVLLYIDRLVHEVTSPOAFEGILRNAGRKVRBPDCLTATTD	68	
DB	3	KTIYERKLFDAHVVEAENETPLLYIDRLVHEVTSPOAFDGLRAGRVRQCKTPTATMD	62	
QY	69	HNVPTTRKALKDIASFKEPDSRQCVTLEENVKEFGVTYEGLSDKRCQIVHVIGPEQG	128	
DB	63	HNVSTQ----KQINAC--GEMAIQMOELIKCKEFGVELYDLNHPYQIGIVHVMGPEQG	116	
QY	129	FTLPPTTVVCGDSTHTSHGAFALAFEGITSEVEHLVATQCLITTKRSKNMRIQVDELAP	188	
DB	117	VTLPGMTIVGDSSTATHGAFALAFEGITSEVEHLVATQCLKGRATKMKLEVOGKAAP	176	
QY	189	GVESKDVVLAAIGITAGTGAVTEFCGYSITRSLSMARNSICMSTEGCARAGVAVD	248	
DB	177	GIKAKOIVLAIIGKTSAGGTGHVFEQGEAIROLSMGGRMTLCMALEMGAAGVAVD	236	
QY	249	ETTFEYIKGFLPAFKYDSPENHKATQYKMLQSPDGAKYDIDFIDAKDIVEFTLTWGTSP	308	
DB	237	ETTFENVYKGLHAPK--GKQFDQDAVAAWKTLQTDGAFDFPVVTLQAAEISISQVWTGTP	294	
QY	309	EDVVPITGVVPDETEFAETKAKDGRMLQYMGKAGTPMEDIPVDKFIQSCNTRIAD	368	
DB	295	GVYISVNDNIPDPSAFDPYERASAEKALAVMGILKPGILLREVALDVKFIQSCNTRIAD	354	
QY	369	LRPAAAVVGRKKAPNVKSLMVPVPGSLVYTOAEPEGIDKTFEENAGFEWRREAGSCMCLG	428	
DB	355	LRPAALYLAKGRKAPAGQV-ALVVPGSGPVKAQAAEAGIDKTFIEGFEWRRLPGSCMCLAM	413	
QY	429	NPDILAPQERCASTSNRNFEGROGAGRTHLMSPVMAAAGIVGLTADVRKL	480	
DB	414	NNDRILNPERCASTSNRNFEGROGGRTHLVSPAMAAAAAVTGHPADIRNI	465	
RESULT 18				
A10065				
3-isopropylmalate dehydratase (EC 4.2.1.33) large chain [imported] - Yersinia pestis (str				
C/S/Species: Yersinia pestis				
C/Date: 02-Nov-2001 #sequence _revision 02-Nov-2001 #text _change 27-Nov-2001				
J/Accession: A10065				

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Versinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: A10085  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-476 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89388.1; PID:g15978624; GSPDB:GN00175  
C:Genetics:  
C:Superfamily: aconitate hydratase  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 35.8%; Score 1452; DB 2; Length 476;  
Best Local Similarity 59.2%; Pred. No. 8.2e-94;  
Matches 289; Conservative 66; Mismatches 121; Indels 12; Gaps 5;  
QY 1 MPGAESTPOTLYDKVLQAHVDEKLDGTLLYIDRLHVEVTSPOAFGLRNAGRKVRP 60  
DB 1 MGTSSQSKTLQKLYDAHIVHEAPNETPLLYIDRLHVEVTSPOAFGLRNAGRPVRQ 60  
QY 61 DCLATTDNHNPVTSRKALKDIASFIEDDRTQCVTLNENKFEVTVFGLSKRGIV 120  
DB 61 GKTFTMDHNVSTQ-----KDINA--SGEWARIQMQLINKCAEFGVSLVDLHNPFGIV 114  
QY 121 HVIGPQGTFLPGTTVVGDSHTSTHGAFCALAFGIGTSEVHVLATQCLITKRSKNM 180  
DB 115 HVIGPQGTFLPGTTVVGDSHTSTHGAFCALAFGIGTSEVHVLATQCLITKRSKNM 174  
QY 181 QVDGELAPGVSSKDVVLHAIIGITAGGTGAVTEFCGVSIRLSMEARMSICNMSIEGGA 240  
DB 175 EVNGTVGAGITAKIDVLAIGTGSAGTGAVTEFCGVSIRLSMEARMSICNMSIEGGA 234  
QY 241 RAGMVAPEITTEFLYKGRPLAPKYDSEVHKATQYWKNLQSDPGAKYDIDVFDIAK 300  
DB 235 KAGLAPADDTTFAYLKGRQFAP--TGQWEGGVAVWYRLKSDADAFDTITLDAADIAP 292  
QY 301 TLTWGTSPDVVPTGVVPPDPTFATEAKADGRMLQYMKLAKGTWEDIPVDKVF 360  
DB 293 QVTWGTNPGQVIAVQIIPAPESFSDVERASAEKALAYMDLRFQIKLVEAIDKVF 352  
QY 361 CTNSRIEDLRAAAVVKRKKAPNVKSAMVPGSLVKTQAEELGDKIPPEAGFEWREA 420  
DB 353 CTNSRIEDLRAAAVVKRKKAPNVKSAMVPGSLVKTQAEELGDKIPPEAGFEWREA 411  
QY 421 GCSMCLGMNPDILAPQERCASTSNRNFEGRQAGGRTHLMSPVMAAAAGIVGKLADVR 480  
DB 412 GCSMCLAMNDRLEPGERCASTSNRNFEGRQAGGRTHLMSPVMAAAAGIVGKLADVR 471  
QY 481 TDYKASPH 488  
DB 472 S---ATTH 476

RESULT 19  
H82070  
3-isopropylmalate dehydratase, large chain VC2492 [similarity] - *Vibrio cholerae* (strain  
C:Species: *Vibrio cholerae*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C:Accession: H82070  
R;Heideberg, D.; Ermolaeva, M.D.; Vanathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B.  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: H82070  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-467 <HEI>

A:Cross-references: GB:AE004318; GB:AE003852; NID:g9657063; PIDN:AAF5634.1; GSPDB:G  
A:Experimental source: serogroup O1; strain N16961; biotype E1 for  
C:Genetics:  
A:Gene: VC2492  
A:Map position: 1  
C:Superfamily: aconitate hydratase

Query Match 35.2%; Score 1425.5; DB 2; Length 467;  
Best Local Similarity 58.9%; Pred. No. 5.7e-92;  
Matches 279; Conservative 67; Mismatches 119; Indels 9; Gaps 4;  
QY 6 STQOTLYDKVLQAHVDEKLDGTLLYIDRLHVEVTSPOAFGLRNAGRKVRPDC 65  
DB 2 SKATLYEKIYDAHVVAAPGETPILYIDRLHVEVTSPOAFGLRNAGRKVRPDC 61  
QY 66 TTDHNPVTSRKALKDIASFIEDDRTQCVTLNENKFEVTVFGLSKRGIV 125  
DB 62 TMDHNVSTTT-----KDINA--SGEWARIQMQLINKCAEFGVSLVDLHNPFGIV 115  
QY 126 EQGFTLPGTTVVGDSHTSTHGAFCALAFGIGTSEVHVLATQCLITKRSKNM 185  
DB 116 ELGITLPGMTIVCGDSHTATGAFGLAFGIGTSEVHVLATQCLITKRSKNM 175  
QY 186 LAPGVSSKDVVLHAIIGITAGGTGAVTEFCGVSIRLSMEARMSICNMSIEGGA 245  
DB 176 VAPGITAKIDVLAIGTGAAGGTGAVTEFCGVSIRLSMEARMSICNMSIEGGA 235  
QY 246 APDITTEYLKGRPLAPKYDSEVHKATQYWKNLQSDPGAKYDIDVFDIAK 305  
DB 236 APDATTNNYIKGRQFAPQ--GSDWDAVDMYQTLTDEDAQFDVAVTLEASEIKPQ 293  
QY 306 TSPEDVVPITGVVPPDPTFATEAKADGRMLQYMKLAKGTWEDIPVDKVF 365  
DB 294 TNPQGVIAVDEPISPSQFADPVERASAEKALAYMDLRFQIKLVEAIDKVF 353  
QY 366 IEDLRAAAVVKRKKAPNVKSAMVPGSLVKTQAEELGDKIPPEAGFEWREAGCSMC 425  
DB 354 IEDMRAAAVVKRKKAPNVKSAMVPGSLVKTQAEELGDKIPPEAGFEWREAGCSMC 412  
QY 426 LGMPNDIILAPQERCASTSNRNFEGRQAGGRTHLMSPVMAAAAGIVGKLADVR 479  
DB 413 LAMNDRLEPGERCASTSNRNFEGRQAGGRTHLMSPVMAAAAGIVGKLADVR 466

RESULT 20  
I39699  
3-isopropylmalate dehydratase (EC 4.2.1.33) large chain - *Actinoplanes teichomycetic*  
N:Alternate names: isopropylmalate isomerase large chain  
C:Species: *Actinoplanes teichomyceticus*  
C:Date: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 24-Nov-1999  
C:Accession: I39699  
R;Castelli, P.; Donadio, S.; Marinelli, F.; Borghi, A.; Sosio, M.  
Gene 158, 97-100, 1995  
A:Title: Complementatation of a *Streptomyces lividans* Leu- mutant by the *Actinoplanes*  
A:Reference number: I39699; MUID:95309734; PMID:7789819  
A:Accession: I39699  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-485 <RES>  
A:Cross-references: EMBL:X84647; NID:g1008941; PIDN:CAA59140.1; PID:g1008942  
A:Experimental source: ATCC 31121  
C:Genetics:  
A:Gene: leuC  
A:Function:  
A:Pathway: leucine biosynthesis  
C:Superfamily: aconitate hydratase  
C:Keywords: 4Fe-4S; carbon-oxygen lyase; hydro-lyase; iron-sulfur protein; leucine  
P:367,427,430/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 34.8%; Score 1413; DB 2; Length 485;  
Best Local Similarity 59.7%; Pred. No. 4.6e-91;  
Matches 285; Conservative 51; Mismatches 125; Indels 16; Gaps 5;

Oy 248 DDTITTEYLKGRPLAPKYDSEEMHKATQYWKNGLOSDPGAKVIDVFDIDAKDLVPILTWTGS 307  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 236 DSVTETVEYLGSRPAAPGGEA--PDVAIQOWEALATDAQAVDVRLTMAASEIEPMWTTGN 293  
Oy 308 PEDVDVITGVDPPEPFATPATAKKADGRMLQYMGLKKGTPEMDI PVDKVFPIGSCNNRTE 367  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 294 PAGCGIVSQVVNSPDDAKDENERRATKQSIAVMGLEGTPTFTETAIQHVFIFGSCNRSLS 353  
Oy 368 DLRAAAVVKGRKKKAPNVKSAMVYPGSGLYKTQAEEBGLDXIFEAEAGEWEAGSCMCIG 427  
Db 354 DLRTAEELIKGRVADAGVR-ALVVPSSQQYKRAAEKGSLDEIFFEAGEFEMWDSCGSMCLG 412  
Oy 428 NMPDILAPDERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAAGIVYKLADV 478  
Db 413 NMDFVPEGERCASTSNRNFEGRQGKGRKTRHLVSFPMAAAAAAGHFVDVR 463

RESULT 22  
B69650  
3-isopropylmalate dehydratase (EC 4.2.1.33) large chain - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C:Accession: B69650  
R:Kunst, F., Ogasaara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Beterer, C.; Bron, S.; Bröhlert, S.; Brunsch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gallier, L.; Harwood, C.R.; Hensut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hulio, M.F.; Koether, P.; Königstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidis, A.; Lardinois, A.; Authors: Lauber, J.; Lazarovic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akenuhi, M.; Yamakoshi, A.; Tanaka, T.; Tepstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winfers, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumsen, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MWID:P98044033; PMID:9384377  
A:Accession: B69650  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-472 <KUN>  
A:Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14786.1; PID:g2635291  
A:Experimental source: strain 168  
A:Gene: leuc  
C:Genetics:  
C:Function:  
A:Pathway: leucine biosynthesis  
C:Superfamily: acornitate hydratase  
C:Keywords: 4fe-4S carbon-oxygen lyase, hydro-lyase, iron-sulfur protein, leucine biosyn /347,407,410/Binding site: 4fe-4S cluster (Cys) (covalent) #status predicted

	Query Match	34.4%	Score 1393.5;	DB 2;	Length 472;
	Best Local Similarity	56.5%	Pred. No. 1e-89;		
	Matches 277; Conservative	63;	Mismatches 129;	Indels 21;	Gaps 4;
Qy	8	PQTLDKYLQAAMVEDEKLDGTGLVLTIDRLVHEVTSPOAFEGEGRNAGRKRVRPDTLATT	67		
	:	:::			
Dd	3	PTTIEKEIMDGIIVHGGEKKPDLLYIDLHLIHEVTSPOAFEGELRQRKRKYRRPPONTFATM	62		
	:	:::			
Qy	68	DHNVPTSRKALKDIASFKEEDDSRTQCVTLEENVKEFGVTVYGSLDRQGCIHVHIGPEQ	127		
	:	:::			
Dd	63	DHNLETNRFEFKD-----EVAKRQVTALERNCEEFGRRLADLHSDGIVAHVGDEL	115		
	:	:::			
Qy	128	GFTLPGETVTCGDSSHSTHTSGAFCALAFGIGTSEVEAVLATQCLITRSKNMRIQVDGELA	187		
	:	:::			
Dd	116	GLTLPGKTIIVCCDSHTSHTGAFGALAFGIGTSEVENHLSQTLMQRPXILEVAVDGTLQ	175		
	:	:::			
Qy	188	PGVSKDVVLHAIGITIAGTAGTAVIDFCGSVIRLSLMEARMSICNNISLEGARAGNAVAP	247		
	:	:::			
Dd	176	KGVAKDAVILVITGKRYGVKFGTGVLEYTGEVFRRNTMTBERMTVCNNISLAGAAAGLIAP	235		
	:	:::			





